

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/619,685A  
Source: IFW/B  
Date Processed by STIC: 07-19-2005

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 07/19/2005

PATENT APPLICATION: US/10/619,685A

TIME: 11:06:22

Input Set : A:\Yam20052.txt

Output Set: N:\CRF4\07192005\J619685A.raw

3 <110> APPLICANT: National Institute of Agrobiological Resources, Ministry of Agriculture,

4 Forestry and Fisheries

5 Japan Science and Technology Corporation

7 <120> TITLE OF INVENTION: A NOVEL GENE FOR CONTROLLING LEAF SHAPES

W--> 9 <130> FILE REFERENCE:

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/619,685A

C--> 12 <141> CURRENT FILING DATE: 2003-07-15

14 <160> NUMBER OF SEQ ID NOS: 15

16 <170> SOFTWARE: PatentIn Ver. 2.1

18 <210> SEQ ID NO: 1

19 <211> LENGTH: 2468

20 <212> TYPE: DNA

21 <213> ORGANISM: Oryza sativa

23 <220> FEATURE:

24 <221> NAME/KEY: CDS

25 <222> LOCATION: (198)..(2270)

27 <300> PUBLICATION INFORMATION:

29 <400> SEQUENCE: 1

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34 gccgccccgt ctgcctctcc ccgctcgacg agaccgcgcc gaggcgcgaa gaggcctagt 180
36 gttcttcgca cctcgcg atg agt agc gcg gtg aag gac cag ctt cac cag 230
37 Met Ser Ser Ala Val Lys Asp Gln Leu His Gln
38 1 5 10
40 atg tcg acg aca tgc gat tcg ctt cta ctg gag ctc aat gtg att tgg 278
41 Met Ser Thr Thr Cys Asp Ser Leu Leu Glu Leu Asn Val Ile Trp
42 15 20 25
44 gat gag gtc ggt gag ccc gac acg acg agg gac agg atg ctg ctg gag 326
45 Asp Glu Val Gly Glu Pro Asp Thr Thr Arg Asp Arg Met Leu Leu Glu
46 30 35 40
49 ctc gag cag gag tgc ctg gag gtc tac agg cgg aag gtc gac cag gcg 374
50 Leu Glu Gln Glu Cys Leu Glu Val Tyr Arg Arg Lys Val Asp Gln Ala
51 45 50 55
53 aac cgg agc cgc gcc cag ctg cgg aag gcc atc gcc gag ggc gag gca 422
54 Asn Arg Ser Arg Ala Gln Leu Arg Lys Ala Ile Ala Glu Gly Glu Ala
55 60 65 70 75
59 gag ctc gcc ggc atc tgc tca gcc atg ggc gag ccg ccc gtg cac gtt 470
60 Glu Leu Ala Gly Ile Cys Ser Ala Met Gly Glu Pro Pro Val His Val
61 80 85 90
63 aga cag tca aat cag aag ctt cat ggc tta aga gag gag ttg aat gca 518
64 Arg Gln Ser Asn Gln Lys Leu His Gly Leu Arg Glu Glu Leu Asn Ala
65 95 100 105
67 att gtt ccg tat ttg gaa gaa atg aaa aag aaa aag gtc gaa cga tgg 566

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68 Ile Val Pro Tyr Leu Glu Glu Met Lys Lys Lys Lys Val Glu Arg Trp
69          110          115          120
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72 Asn Gln Phe Val His Val Ile Glu Gln Ile Lys Lys Ile Ser Ser Glu
73      125          130          135
75 ata agg cca gcc gat ttt gtt ccc ttt aaa gtt ccg gtt gat cag tct 662
76 Ile Arg Pro Ala Asp Phe Val Pro Phe Lys Val Pro Val Asp Gln Ser
77 140          145          150          155
79 gac ctg tca tta aga aag ctt gat gag ttg acg aag gac ctg gaa tcc 710
80 Asp Leu Ser Leu Arg Lys Leu Asp Glu Leu Thr Lys Asp Leu Glu Ser
81          160          165          170
83 ctt cag aag gag aag agc gat cgg cta aag caa gtg ata gaa cat ttg 758
84 Leu Gln Lys Glu Lys Ser Asp Arg Leu Lys Gln Val Ile Glu His Leu
85          175          180          185
87 aat tct ttg cat tcc tta tgt gag gtg ctt ggc ata gat ttc aag caa 806
88 Asn Ser Leu His Ser Leu Cys Glu Val Leu Gly Ile Asp Phe Lys Gln
89      190          195          200
91 aca gta tat gag gtg cac cct agc ttg gac gaa gct gaa gga tca aag 854
92 Thr Val Tyr Glu Val His Pro Ser Leu Asp Glu Ala Glu Gly Ser Lys
93      205          210          215
95 aac ctg agc aac act aca att gag agg ctt gct gct gcc gca aac aga 902
96 Asn Leu Ser Asn Thr Thr Ile Glu Arg Leu Ala Ala Ala Ala Asn Arg
97 220          225          230          235
99 ctg cgt gaa atg aag atc caa agg atg caa aag ctt caa gat ttt gct 950
100 Leu Arg Glu Met Lys Ile Gln Arg Met Gln Lys Leu Gln Asp Phe Ala
101          240          245          250
103 tct agc atg ctc gag cta tgg aat ctc atg gat act cca ctt gaa gag 998
104 Ser Ser Met Leu Glu Leu Trp Asn Leu Met Asp Thr Pro Leu Glu Glu
105          255          260          265
107 cag cag atg ttt cag aat ata aca tgc aat att gct gct tca gaa caa 1046
108 Gln Gln Met Phe Gln Asn Ile Thr Cys Asn Ile Ala Ala Ser Glu Gln
109      270          275          280
111 gag ata act gaa cca aac acc ctc tcc aca gat ttc ctg aat tat gtc 1094
112 Glu Ile Thr Glu Pro Asn Thr Leu Ser Thr Asp Phe Leu Asn Tyr Val
113      285          290          295
117 gaa tct gag gtg tta agg ctt gaa caa ctg aaa gca agt aag atg aaa 1142
118 Glu Ser Glu Val Leu Arg Leu Glu Gln Leu Lys Ala Ser Lys Met Lys
119 300          305          310          315
121 gat ctt gtt tta aaa aag aaa gca gaa cta gaa gag cat aga aga cgt 1190
122 Asp Leu Val Leu Lys Lys Lys Ala Glu Leu Glu Glu His Arg Arg Arg
123          320          325          330
125 gct cat ctt gtt ggc gag gaa ggt tat gca gag gag ttt agc att gaa 1238
126 Ala His Leu Val Gly Glu Glu Gly Tyr Ala Glu Glu Phe Ser Ile Glu
127          335          340          345
129 gct att gaa gct gga gct att gat ccc tca cta gta ctt gaa caa att 1286
130 Ala Ile Glu Ala Gly Ala Ile Asp Pro Ser Leu Val Leu Glu Gln Ile
131      350          355          360
133 gaa gct cac att gca aca gtg aaa gag gaa gct ttt agc cgg aag gat 1334
134 Glu Ala His Ile Ala Thr Val Lys Glu Glu Ala Phe Ser Arg Lys Asp

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137	att ctt gag aaa gtt gaa aga tgg caa aat gct tgt gaa gag gaa gcc	1382		
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139	380 385 390 395			
141	tgg ctg gaa gat tac aac aaa gat gat aat cgt tac aat gct ggg agg	1430		
142	Trp Leu Glu Asp Tyr Asn Lys Asp Asp Asn Arg Tyr Asn Ala Gly Arg			
143	400 405 410			
145	gga gca cat cta aca cta aag agg gct gaa aag gct cgt act ttg gtc	1478		
146	Gly Ala His Leu Thr Leu Lys Arg Ala Glu Lys Ala Arg Thr Leu Val			
147	415 420 425			
149	aac aag att cct gga atg gta gat gtt ttg aga aca aaa att gct gca	1526		
150	Asn Lys Ile Pro Gly Met Val Asp Val Leu Arg Thr Lys Ile Ala Ala			
151	430 435 440			
153	tgg aaa aat gaa cga gga aag gag gat ttc aca tat gat ggt gtt agc	1574		
154	Trp Lys Asn Glu Arg Gly Lys Glu Asp Phe Thr Tyr Asp Gly Val Ser			
155	445 450 455			
157	ctt tcg tca atg ctt gat gaa tat atg ttc gtt cgt cag gag aaa gag	1622		
158	Leu Ser Ser Met Leu Asp Glu Tyr Met Phe Val Arg Gln Glu Lys Glu			
159	460 465 470 475			
161	caa gag aag aag aga caa agg gat cag aag aag ctc cag gat cag ctc	1670		
162	Gln Glu Lys Lys Arg Gln Arg Asp Gln Lys Lys Leu Gln Asp Gln Leu			
163	480 485 490			
165	aaa gcg gag cag gaa gct ttg tac gga tca aaa ccc agt cca tcc aag	1718		
166	Lys Ala Glu Gln Glu Ala Leu Tyr Gly Ser Lys Pro Ser Pro Ser Lys			
167	495 500 505			
169	ccc cta agt aca aag aag gca cct agg cac tct atg ggt ggt gca aac	1766		
170	Pro Leu Ser Thr Lys Lys Ala Pro Arg His Ser Met Gly Gly Ala Asn			
171	510 515 520			
175	cga agg cta tct ctt ggt gga gcc acc atg caa ccc ccg aag act gat	1814		
176	Arg Arg Leu Ser Leu Gly Gly Ala Thr Met Gln Pro Pro Lys Thr Asp			
177	525 530 535			
179	ata ctg cat tca aag tct gtt cgt gct gcc aag aaa act gaa gaa atc	1862		
180	Ile Leu His Ser Lys Ser Val Arg Ala Ala Lys Lys Thr Glu Glu Ile			
181	540 545 550 555			
183	ggc act ttg tcc cct agt agt aga ggt ttg gac att gcc gga ttg	1910		
184	Gly Thr Leu Ser Pro Ser Ser Ser Arg Gly Leu Asp Ile Ala Gly Leu			
185	560 565 570			
187	cct atc aag aag ttg tct ttc aat gcc agt act cta cgt gag acg gag	1958		
188	Pro Ile Lys Lys Leu Ser Phe Asn Ala Ser Thr Leu Arg Glu Thr Glu			
189	575 580 585			
191	aca cct cgt aaa cct ttt gct cag atc aca cca gga aac agt gtc tcg	2006		
192	Thr Pro Arg Lys Pro Phe Ala Gln Ile Thr Pro Gly Asn Ser Val Ser			
193	590 595 600			
195	tcg acg cct gtg cgc cct atc acc aat aac act gag gat gat gag aac	2054		
196	Ser Thr Pro Val Arg Pro Ile Thr Asn Asn Thr Glu Asp Asp Glu Asn			
197	605 610 615			
199	agg act ccg aag aca ttt aca gca ctg aat ccc aag act ccg atg act	2102		
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201	620 625 630 635			

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207 gtt tca gca act cca gtt tcc ctt gtt tac gac aag cca gag gta aca      2198
208 Val Ser Ala Thr Pro Val Ser Leu Val Tyr Asp Lys Pro Glu Val Thr
209          655          660          665
211 ttg cag gag gac atc gac tac tcc ttt gaa gaa agg cgg ctc gcc atc      2246
212 Leu Gln Glu Asp Ile Asp Tyr Ser Phe Glu Glu Arg Arg Leu Ala Ile
213          670          675          680
215 tat ctg gcc agg caa atg gtt taa ctgttgatca atttatgtac gtagttgaaa      2300
216 Tyr Leu Ala Arg Gln Met Val
217          685          690
219 tctgactgca ttttcttgct ggtggccatt gcgtatgttg gtcaacaata gtcggccttt      2360
221 ccagtagcac tattctgatt tactgcaatt gttttaatgt tttctacaac cagtaaaaca      2420
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226 <211> LENGTH: 690
227 <212> TYPE: PRT
228 <213> ORGANISM: Oryza sativa
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234          20          25          30
235 Pro Asp Thr Thr Arg Asp Arg Met Leu Leu Glu Leu Glu Gln Glu Cys
236          35          40          45
237 Leu Glu Val Tyr Arg Arg Lys Val Asp Gln Ala Asn Arg Ser Arg Ala
238          50          55          60
239 Gln Leu Arg Lys Ala Ile Ala Glu Gly Glu Ala Glu Leu Ala Gly Ile
240   65          70          75          80
241 Cys Ser Ala Met Gly Glu Pro Pro Val His Val Arg Gln Ser Asn Gln
242          85          90          95
243 Lys Leu His Gly Leu Arg Glu Glu Leu Asn Ala Ile Val Pro Tyr Leu
244          100          105          110
245 Glu Glu Met Lys Lys Lys Lys Val Glu Arg Trp Asn Gln Phe Val His
246          115          120          125
247 Val Ile Glu Gln Ile Lys Lys Ile Ser Ser Glu Ile Arg Pro Ala Asp
248          130          135          140
249 Phe Val Pro Phe Lys Val Pro Val Asp Gln Ser Asp Leu Ser Leu Arg
250 145          150          155          160
251 Lys Leu Asp Glu Leu Thr Lys Asp Leu Glu Ser Leu Gln Lys Glu Lys
252          165          170          175
253 Ser Asp Arg Leu Lys Gln Val Ile Glu His Leu Asn Ser Leu His Ser
254          180          185          190
255 Leu Cys Glu Val Leu Gly Ile Asp Phe Lys Gln Thr Val Tyr Glu Val
256          195          200          205
257 His Pro Ser Leu Asp Glu Ala Glu Gly Ser Lys Asn Leu Ser Asn Thr
258          210          215          220
259 Thr Ile Glu Arg Leu Ala Ala Ala Asn Arg Leu Arg Glu Met Lys

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264				260					265					270		
265	Asn	Ile	Thr	Cys	Asn	Ile	Ala	Ala	Ser	Glu	Gln	Glu	Ile	Thr	Glu	Pro
266			275					280					285			
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268		290					295					300				
269	Arg	Leu	Glu	Gln	Leu	Lys	Ala	Ser	Lys	Met	Lys	Asp	Leu	Val	Leu	Lys
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271	Lys	Lys	Ala	Glu	Leu	Glu	Glu	His	Arg	Arg	Arg	Ala	His	Leu	Val	Gly
272				325					330					335		
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274			340						345					350		
275	Ala	Ile	Asp	Pro	Ser	Leu	Val	Leu	Glu	Gln	Ile	Glu	Ala	His	Ile	Ala
276			355					360					365			
277	Thr	Val	Lys	Glu	Glu	Ala	Phe	Ser	Arg	Lys	Asp	Ile	Leu	Glu	Lys	Val
278		370					375					380				
279	Glu	Arg	Trp	Gln	Asn	Ala	Cys	Glu	Glu	Glu	Ala	Trp	Leu	Glu	Asp	Tyr
280	385					390					395				400	
281	Asn	Lys	Asp	Asp	Asn	Arg	Tyr	Asn	Ala	Gly	Arg	Gly	Ala	His	Leu	Thr
282				405						410				415		
283	Leu	Lys	Arg	Ala	Glu	Lys	Ala	Arg	Thr	Leu	Val	Asn	Lys	Ile	Pro	Gly
284			420						425				430			
285	Met	Val	Asp	Val	Leu	Arg	Thr	Lys	Ile	Ala	Ala	Trp	Lys	Asn	Glu	Arg
286			435					440					445			
287	Gly	Lys	Glu	Asp	Phe	Thr	Tyr	Asp	Gly	Val	Ser	Leu	Ser	Ser	Met	Leu
288		450					455					460				
289	Asp	Glu	Tyr	Met	Phe	Val	Arg	Gln	Glu	Lys	Glu	Gln	Glu	Lys	Lys	Arg
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291	Gln	Arg	Asp	Gln	Lys	Lys	Leu	Gln	Asp	Gln	Leu	Lys	Ala	Glu	Gln	Glu
292				485						490				495		
293	Ala	Leu	Tyr	Gly	Ser	Lys	Pro	Ser	Pro	Ser	Lys	Pro	Leu	Ser	Thr	Lys
294			500						505				510			
295	Lys	Ala	Pro	Arg	His	Ser	Met	Gly	Gly	Ala	Asn	Arg	Arg	Leu	Ser	Leu
296			515					520					525			
297	Gly	Gly	Ala	Thr	Met	Gln	Pro	Pro	Lys	Thr	Asp	Ile	Leu	His	Ser	Lys
298		530					535					540				
299	Ser	Val	Arg	Ala	Ala	Lys	Lys	Thr	Glu	Glu	Ile	Gly	Thr	Leu	Ser	Pro
300	545					550					555				560	
301	Ser	Ser	Ser	Arg	Gly	Leu	Asp	Ile	Ala	Gly	Leu	Pro	Ile	Lys	Lys	Leu
302				565						570				575		
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304			580						585				590			
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306			595					600					605			
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308		610					615					620				

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L:9 M:201 W: Mandatory field data missing, <130> FILE REFERENCE

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date